

# Complete Genome Sequence of a *Brucella ceti* ST26 Strain Isolated from a Striped Dolphin (*Stenella coeruleoalba*) on the Coast of Italy

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***Brucella* spp. are important pathogens affecting a wide range of terrestrial and aquatic animals. We report the complete and annotated genome sequence of *Brucella ceti* ST26 strain TE10759-12, isolated from a striped dolphin (*Stenella coeruleoalba*) stranded along the Italian shoreline in March of 2012.**

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**B**rucella spp. are facultative intracellular bacteria causing brucellosis, which is a worldwide-occurring zoonotic disease characterized by abortion in domestic animals and undulant fever, arthritis, endocarditis, and meningitis in humans. *Brucella* spp. comprise six classical (*B. abortus*, *B. melitensis*, *B. suis*, *B. ovis*, *B. canis*, and *B. neotomae*) and four novel (*B. ceti*, *B. pinnipedialis*, *B. inopinata*, and *B. microti*) species infecting terrestrial and aquatic animals (1). The genome of *Brucella* is composed of two circular chromosomes without any plasmids. An identity of >90% has been described among the genomes of the six classical species (1). Marine brucellosis has been recognized as a serious threat to seals, sea lions, walruses, dolphins, porpoises, and whales. Two *Brucella* species are recognized in marine mammals, including *B. ceti* from cetaceans and *B. pinnipedialis* from pinnipeds (2). However, cross-species infections may also occur, and zoonotic transmission cannot be ruled out (3). Since 1994, when *B. ceti* was first isolated from an aborted dolphin fetus, several cases have been reported worldwide (2). *B. ceti* strain TE10759-12 was isolated from a striped dolphin (*Stenella coeruleoalba*) stranded on the southern coastline of Apulia in 2012 (4). In recent years, with the implementation of sequencing strategies, more whole genome sequences of *Brucella* have become publicly available. However, except for scaffold sequences from three isolates (5), whole-genome sequences of *B. ceti* have not been available. Here, we announce the complete genome sequence of *B. ceti* ST26 strain TE10759-12, with the sequencing performed at the Istituto Zooprofilattico Sperimentale dell'Abruzzo e Molise G. Caporale in Teramo, Italy. This strain was previously characterized through multilocus sequence typing (MLST) analysis as belonging to the common sequence type 26 (ST26), while by multilocus variable-number tandem-repeat analysis (MLVA) of 16 loci, it was demonstrated to represent a genotype within cluster A (4). *B. ceti* ST26 is the most common *B. ceti* sequence type isolated from dolphins worldwide (2). Whole-genome sequencing of strain TE10759-12 was performed using an Ion Torrent PGM platform (~230-bp single-end library with ~20-fold coverage). The reads were *de novo*

assembled using Velvet software version 1.1.0 (6). The genomes were finished by in-house-developed Python packages. Genome annotation was performed by Prokka, followed by manual inspection. The whole genome of strain TE10759-12 was demonstrated to have a G+C content of 57%, and it is composed of chromosomes 1 and 2, which are 2,117,718 and 1,160,316 bp, respectively. Furthermore, 9 complete rRNAs, 44 tRNAs operons, and 2,611 coding sequences (CDSs) were also described. In this report, the first complete genome sequence for *B. ceti* ST26 has been described, and it represents a crucial achievement for further studies on the evolution, epidemiology, and pathogenicity of this cluster of *Brucella*.

**Nucleotide sequence accession numbers.** The complete genome of *B. ceti* TE10759-12 has been deposited in GenBank with the accession no. [CP006896](http://dx.doi.org/10.1128/genomeA.00068-14) for chromosome 1 and [CP006897](http://dx.doi.org/10.1128/genomeA.00068-14) for chromosome 2.

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The mention of trade names or commercial products in this article is solely for the purpose of providing specific information and does not imply recommendation or endorsement by the OIE Reference Laboratory for Brucellosis in Teramo.

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